



-1-

SEQUENCE LISTING

<110> Gardella, Thomas J.  
Kronenberg, Henry M.  
Potts, John T.  
Juppner, Harald

<120> PTH Functional Domain Conjugate Peptides, Derivatives  
Thereof and Novel Tethered Ligand-Receptor Molecules

<130> 0609.4780001

<140> US 09/475,158  
<141> 1999-12-30

<150> US 60/114,577  
<151> 1998-12-31

<160> 74

<170> PatentIn Ver. 2.1

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<212> PRT  
<213> Homo sapiens

<400> 1  
Ala Val Ser Glu Ile Gln Leu Met His  
1 5

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<211> 17  
<212> PRT  
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1 5 10 15

Val

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<211> 31  
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<213> Artificial Sequence

<220>  
<223> modified PTH sequence

<400> 3

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1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val

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25

30

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<213> Homo sapiens

<400> 4  
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1 5

<210> 5  
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<220>  
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Ala Val Ser Glu Ile Gly Gly Gly Gly Gly Gly Gly Leu Asn  
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> modified PTH sequence

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Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Gly  
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val  
20 25 30

<210> 7  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 7  
Ala Val Ser Glu His Gln Leu Leu His  
1 5

<210> 8  
<211> 17

<212> PRT  
<213> Homo sapiens

<400> 8  
Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu  
1 5 10 15

Ile

<210> 9  
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<213> Artificial Sequence

<220>  
<223> modified PTH sequence

<220>  
<221> MOD\_RES  
<222> (31)..(31)  
<223> AMIDATION

<400> 9  
Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Leu Asn  
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val  
20 25 30

<210> 10  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 10  
Ala Val Ser Glu His  
1 5

<210> 11  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> modified PTH sequence

<220>  
<221> MOD\_RES  
<222> (31)..(31)  
<223> AMIDATION

<400> 11

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Gly  
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val  
20 25 30

<210> 12  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 12  
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile  
1 5 10 15

<210> 13  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> modified PTH sequence

<220>  
<221> MOD\_RES  
<222> (31)..(31)  
<223> AMIDATION

<400> 13

Ala Val Ser Glu Ile Gly Gly Gly Gly Gly Gly Gly Leu Asn  
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val  
20 25 30

<210> 14  
<211> 93  
<212> RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 14  
gcuguuuccg aaauccagcu gaugcacggu ggugguggug gucugaacuc cauggaacgu 60  
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 15  
<211> 93

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH sequence

<400> 15

gcuguuuccg aaaucaggcu gaugcacggu ggugguggug guggugguuc cauggaacgu 60  
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 16

<211> 93

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH sequence

<400> 16

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guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 17

<211> 34

<212> PRT

<213> Homo sapiens

<400> 17

Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn  
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His  
20 25 30

Asn Phe

<210> 18

<211> 34

<212> PRT

<213> Homo sapiens

<400> 18

Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly Lys Ser Ile Gln  
1 5 10 15

Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile His  
20 25 30

Thr Ala

<210> 19

<211> 37

<212> PRT

<213> Homo sapiens

<400> 19  
His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln  
1 5 10 15  
Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu Gly Lys Arg Tyr Lys  
20 25 30  
Gln Arg Val Asn Lys  
35

<210> 20  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 20  
His Ser Asp Ala Val Phe Thr Asp Asn Tyr Thr Arg Leu Arg Lys Gln  
1 5 10 15  
Met Ala Val Lys Lys Tyr Leu Asn Ser Ile Leu Asn  
20 25

<210> 21  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 21  
Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln  
1 5 10 15  
Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg  
20 25

<210> 22  
<211> 27  
<212> PRT  
<213> Homo sapiens

<400> 22  
His Ala Asp Gly Val Phe Thr Ser Asp Phe Ser Lys Leu Leu Gly Gln  
1 5 10 15  
Leu Ser Ala Lys Lys Tyr Leu Glu Ser Leu Met  
20 25

<210> 23  
<211> 31  
<212> PRT  
<213> Homo sapiens

<400> 23  
His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly  
1 5 10 15  
Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly  
20 25 30

<210> 24  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 24  
His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Ser  
1 5 10 15  
Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr  
20 25

<210> 25  
<211> 42  
<212> PRT  
<213> Homo sapiens

<400> 25  
Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys  
1 5 10 15  
Ile His Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys Gly Lys  
20 25 30  
Lys Asn Asp Trp Lys His Asn Ile Thr Gln  
35 40

<210> 26  
<211> 27  
<212> PRT  
<213> Homo sapiens

<400> 26  
His Ser Asp Gly Thr Phe Thr Ser Glu Leu Ser Arg Leu Arg Glu Gly  
1 5 10 15  
Ala Arg Leu Gln Arg Leu Leu Gln Gly Leu Val  
20 25

<210> 27  
<211> 32  
<212> PRT  
<213> Homo sapiens

<400> 27  
Cys Gly Asn Leu Ser Thr Cys Met Leu Gly Thr Tyr Thr Gln Asp Phe  
1 5 10 15  
Asn Lys Phe His Thr Phe Pro Gln Thr Ala Ile Gly Val Gly Ala Pro  
20 25 30

<210> 28  
<211> 37  
<212> PRT

<213>Homo sapiens

<400> 28  
Ala Cys Asn Thr Ala Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu  
1 5 10 15  
Ser Arg Ser Gly Gly Met Val Lys Ser Asn Phe Val Pro Thr Asn Val  
20 25 30  
Gly Ser Lys Ala Phe  
35

<210> 29  
<211> 37  
<212> PRT  
<213> Homo sapiens

<400> 29  
Ala Cys Asp Thr Ala Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu  
1 5 10 15  
Ser Arg Ser Gly Gly Val Val Lys Asn Asn Phe Val Pro Thr Asn Val  
20 25 30  
Gly Ser Lys Ala Phe  
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<210> 30  
<211> 37  
<212> PRT  
<213>Homo sapiens

<400> 30  
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu  
1 5 10 15  
Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val  
20 25 30  
Gly Ser Asn Thr Tyr  
35

<210> 31  
<211> 36  
<212> PRT  
<213> Homo sapiens

<400> 31  
Gly Cys Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile  
1 5 10 15  
Tyr Gln Phe Thr Asp Lys Asp Asn Val Ala Pro Arg Ser Lys  
20 25 30  
Ile Ser Pro Gln  
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<210> 32

<211> 41  
<212> PRT  
<213> Homo sapiens

<400> 32  
Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg  
1 5 10 15  
Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His  
20 25 30  
Ser Asn Arg Lys Leu Met Glu Ile Ile  
35 40

<210> 33  
<211> 40  
<212> PRT  
<213> Homo sapiens

<400> 33  
Glu Glu Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys  
1 5 10 15  
Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn  
20 25 30  
Asn Arg Leu Leu Leu Asp Thr Ile  
35 40

<210> 34  
<211> 46  
<212> PRT  
<213> Homo sapiens

<400> 34  
Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg  
1 5 10 15  
Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln  
20 25 30  
Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile  
35 40 45

<210> 35  
<211> 63  
<212> PRT  
<213> Homo sapiens

<400> 35  
Cys Asp Ala Thr Cys Gln Phe Arg Lys Ala Ile Asp Asp Cys Gln Lys  
1 5 10 15  
Gln Ala His His Ser Asn Val Leu Gln Thr Ser Val Gln Thr Thr Ala  
20 25 30  
Thr Phe Thr Ser Met Asp Thr Ser Gln Leu Pro Gly Asn Ser Val Phe  
35 40 45

Lys Glu Cys Met Lys Gln Lys Lys Glu Phe Ser Ser Gly Lys  
50 55 60

<210> 36  
<211> 1335  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<220>  
<221> CDS  
<222> (1)..(1332)

<400> 36  
atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc 48  
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys  
1 5 10 15  
cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga 96  
Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly  
20 25 30  
gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac 144  
Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr  
35 40 45  
tcc atg tct ctc gcc tcc ctc acg gtg gct gtg ctc atc ctg gcc tat 192  
Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr  
50 55 60  
ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac atg ttc 240  
Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe  
65 70 75 80  
ctg tcg ttt atg ctg cgc gcc gcg agc atc ttc gtg aag gac gct gtg 288  
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val  
85 90 95  
ctc tac tct ggc ttc acg ctg gat gag gcc gag cgc ctc aca gag gaa 336  
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu  
100 105 110  
gag ttg cac atc atc gcg cag gtg cca cct ccg ccg gcc gct gcc gcc 384  
Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala  
115 120 125  
gta ggc tac gct ggc tgc cgc gtg gcg gtg acc ttc ttc ctc tac ttc 432  
Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe  
130 135 140  
ctg gct acc aac tac tac tgg atc ctg gtg gag ggg ctg tac ttg cac 480  
Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His  
145 150 155 160  
agc ctc atc ttc atg gcc ttt ttc tca gag aag aag tac ctg tgg ggc 528  
Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly  
165 170 175

ttc acc atc ttt ggc tgg ggt cta ccg gct gtc ttc gtg gct gtg tgg	576
Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp	
180 185 190	
gtc ggt gtc aga gca acc ttg gcc aac act ggg tgc tgg gat ctg agc	624
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser	
195 200 205	
tcc ggg cac aag aag tgg atc atc cag gtg ccc atc ctg gca tct gtt	672
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val	
210 215 220	
gtg ctc aac ttc atc ctt ttt atc aac atc atc cgg gtg ctt gcc act	720
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr	
225 230 235 240	
aag ctt cgg gag acc aat gcg ggc cgg tgt gac acc agg cag cag tac	768
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr	
245 250 255	
cgg aag ctg ctc agg tcc acg ttg gtg ctc gtg ccg ctc ttt ggt gtg	816
Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val	
260 265 270	
cac tac acc gtc ttc atg gcc ttg ccg tac acc gag gtc tca ggg aca	864
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr	
275 280 285	
ttg tgg cag atc cag atg cat tat gag atg ctc ttc aac tcc ttc cag	912
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln	
290 295 300	
gga ttt ttt gtt gcc atc ata tac tgt ttc tgc aat ggt gag gtg cag	960
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln	
305 310 315 320	
gca gag att agg aag tca tgg agc cgc tgg aca ctg gcg ttg gac ttc	1008
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe	
325 330 335	
aag cgc aaa gca cga agt ggg agt agc agc tac agc tat ggc cca atg	1056
Lys Arg Lys Ala Arg Ser Gly Ser Ser Tyr Ser Tyr Gly Pro Met	
340 345 350	
gtg tct cac acg agt gtg acc aat gtg ggc ccc cgt gca gga ctc agc	1104
Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser	
355 360 365	
ctc ccc ctc agc ccc cgc ctg cct cct gcc act acc aat ggc cac tcc	1152
Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser	
370 375 380	
cag ctg cct ggc cat gcc aag cca ggg gct cca gcc act gag act gaa	1200
Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu	
385 390 395 400	
acc cta cca gtc act atg gcg gtt ccc aag gac gat gga ttc ctt aac	1248
Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn	
405 410 415	
ggc tcc tgc tca ggc ctg gat gag gag gcc tcc ggg tct gcg cgg ccg	1296
Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro	

420

425

430

cct cca ttg ttg cag gaa gga tgg gaa aca gtc atg tga  
Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met  
435 440

1335

<210> 37  
<211> 444  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<400> 37  
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys  
1 5 10 15  
Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly  
20 25 30  
Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr  
35 40 45  
Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr  
50 55 60  
Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe  
65 70 75 80  
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val  
85 90 95  
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu  
100 105 110  
Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala Ala  
115 120 125  
Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe  
130 135 140  
Leu Ala Thr Asn Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His  
145 150 155 160  
Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly  
165 170 175  
Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp  
180 185 190  
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser  
195 200 205  
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val  
210 215 220  
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr  
225 230 235 240  
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr  
245 250 255  
Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val  
260 265 270  
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr  
275 280 285  
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln  
290 295 300  
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln  
305 310 315 320  
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe  
325 330 335  
Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met  
340 345 350

Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser  
355 360 365  
Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser  
370 375 380  
Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu  
385 390 395 400  
Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn  
405 410 415  
Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro  
420 425 430  
Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met  
435 440

<210> 38  
<211> 1002  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<220>  
<221> CDS  
<222> (1)..(1002)

<400> 38  
atg ggg gcc gcc cggtt atc gca ccc agc ctg gcg ctc cta ctc tgc tgc 48  
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys  
1 5 10 15  
cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga 96  
Pro Val Leu Ser Ser Ala Tyr Ala Glu Thr Ser Glu His Gly Gly  
20 25 30  
gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac 144  
Gly Gly Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr  
35 40 45  
tcc atg tct ctc gcc tcc ctc acg gtg gct gtg ctc atc ctg gcc tat 192  
Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr  
50 55 60  
ttt agg cggtt atg ctg cgc aac tac atc cac atg cac atg ttc 240  
Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe  
65 70 75 80  
ctg tcg ttt atg ctg cgc gcc gcg agc atc ttc gtg aag gac gct gtg 288  
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val  
85 90 95  
ctc tac tct ggc ttc acg ctg gat gag gcc gag cgc ctc aca gag gaa 336  
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu  
100 105 110  
gag ttg cac atc atc gcg cag gtg cca cct ccg ccg gcc gct gcc gcc 384  
Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Ala Ala Ala Ala  
115 120 125  
gta ggc tac gct ggc tgc cgc gtg gcg gtg acc ttc ttc ctc tac ttc 432

Val	Gly	Tyr	Ala	Gly	Cys	Arg	Val	Ala	Val	Thr	Phe	Phe	Leu	Tyr	Phe
130						135					140				
ctg	gct	acc	aac	tac	tac	tgg	atc	ctg	gtg	gag	ggg	ctg	tac	ttg	cac
Leu	Ala	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His
145						150				155				160	
agc	ctc	atc	ttc	atg	gcc	ttt	ttc	tca	gag	aag	aag	tac	ctg	tgg	ggc
Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	Glu	Lys	Lys	Tyr	Leu	Trp	Gly
						165				170			175		528
ttc	acc	atc	ttt	ggc	tgg	ggt	cta	ccg	gct	gtc	ttc	gtg	gct	gtg	tgg
Phe	Thr	Ile	Phe	Gly	Trp	Gly	Leu	Pro	Ala	Val	Phe	Val	Ala	Val	Trp
						180		185				190			576
gtc	ggt	gtc	aga	gca	acc	ttg	gcc	aac	act	ggg	tgc	tgg	gat	ctg	agc
Val	Gly	Val	Arg	Ala	Thr	Leu	Ala	Asn	Thr	Gly	Cys	Trp	Asp	Leu	Ser
						195		200				205			624
tcc	ggg	cac	aag	aag	tgg	atc	atc	cag	gtg	ccc	atc	ctg	gca	tct	gtt
Ser	Gly	His	Lys	Lys	Trp	Ile	Ile	Gln	Val	Pro	Ile	Leu	Ala	Ser	Val
						210		215			220				672
gtg	ctc	aac	ttc	atc	ctt	ttt	atc	aac	atc	atc	cgg	gtg	ctt	gcc	act
Val	Leu	Asn	Phe	Ile	Leu	Phe	Ile	Asn	Ile	Ile	Arg	Val	Leu	Ala	Thr
						225		230			235			240	
aag	ctt	cgg	gag	acc	aat	gcg	ggc	cgg	tgt	gac	acc	agg	cag	cag	tac
Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr	Arg	Gln	Gln	Tyr
						245			250			255			768
cgg	aag	ctg	ctc	agg	tcc	acg	ttg	gtg	ctc	gtg	ccg	ctc	ttt	ggt	gtg
Arg	Lys	Leu	Leu	Arg	Ser	Thr	Leu	Val	Leu	Val	Pro	Leu	Phe	Gly	Val
						260		265			270				816
cac	tac	acc	gtc	ttc	atg	gcc	ttg	ccg	tac	acc	gag	gtc	tca	ggg	aca
His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	Tyr	Thr	Glu	Val	Ser	Gly	Thr
						275		280			285				864
ttg	tgg	cag	atc	cag	atg	cat	tat	gag	atg	ctc	ttc	aac	tcc	ttc	cag
Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	Met	Leu	Phe	Asn	Ser	Phe	Gln
						290		295			300				912
gga	ttt	ttt	gtt	gcc	atc	ata	tac	tgt	ttc	tgc	aat	ggt	gag	gtg	cag
Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly	Glu	Val	Gln
						305		310			315			320	
gca	gag	att	agg	aag	tca	tgg	agc	cgc	tgg	aca	ctg	gcg	tag		
Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala			
						325			330						1002

<210> 39  
<211> 333  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<400> 39  
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys  
1 5 10 15  
Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly  
20 25 30  
Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr  
35 40 45  
Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr  
50 55 60  
Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe  
65 70 75 80  
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val  
85 90 95  
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu  
100 105 110  
Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Ala Ala Ala Ala  
115 120 125  
Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe  
130 135 140  
Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His  
145 150 155 160  
Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly  
165 170 175  
Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp  
180 185 190  
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser  
195 200 205  
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val  
210 215 220  
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr  
225 230 235 240  
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr  
245 250 255  
Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val  
260 265 270  
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr  
275 280 285  
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln  
290 295 300  
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln  
305 310 315 320  
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala  
325 330

<210> 40  
<211> 975  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<220>  
<221> CDS  
<222> (1)...(972)

<400> 40  
atg ggg gcc gcc cggtatc gca ccc agc ctg gcg ctc cta ctc tgc tgc  
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys

1	5	10	15													
cca	gtg	ctc	agc	tcc	gca	tat	gcg	ctg	gag	gta	ttt	gac	cgc	cta	ggc	96
Pro	Val	Leu	Ser	Ser	Ala	Tyr	Ala	Leu	Glu	Val	Phe	Asp	Arg	Leu	Gly	
20								25					30			
atg	atc	tac	acc	gtg	gga	tac	tcc	atg	tct	ctc	gcc	tcc	ctc	acg	gtg	144
Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Met	Ser	Leu	Ala	Ser	Leu	Thr	Val	
35								40					45			
gct	gtg	ctc	atc	ctg	gcc	tat	ttt	agg	cgg	ctg	cac	tgc	acg	cgc	aac	192
Ala	Val	Leu	Ile	Leu	Ala	Tyr	Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	
50								55			60					
tac	atc	cac	atg	cac	atg	ttc	ctg	tcg	ttt	atg	ctg	cgc	gcc	gcg	agc	240
Tyr	Ile	His	Met	His	Met	Phe	Leu	Ser	Phe	Met	Leu	Arg	Ala	Ala	Ser	
65						70				75			80			
atc	ttc	gtg	aag	gac	gct	gtg	ctc	tac	tct	ggc	ttc	acg	ctg	gat	gag	288
Ile	Phe	Val	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Phe	Thr	Leu	Asp	Glu	
85								90					95			
gcc	gag	cgc	ctc	aca	gag	gaa	gag	ttg	cac	atc	atc	gcg	cag	gtg	cca	336
Ala	Glu	Arg	Leu	Thr	Glu	Glu	Glu	Leu	His	Ile	Ile	Ala	Gln	Val	Pro	
100								105					110			
cct	ccg	ccg	gcc	gct	gcc	gta	ggc	tac	gct	ggc	tgc	cgc	gtg	gcg		384
Pro	Pro	Pro	Ala	Ala	Ala	Ala	Val	Gly	Tyr	Ala	Gly	Cys	Arg	Val	Ala	
115							120					125				
gtg	acc	ttc	ttc	ctc	tac	ttc	ctg	gct	acc	aac	tac	tac	tgg	atc	ctg	432
Val	Thr	Phe	Phe	Leu	Tyr	Phe	Leu	Ala	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
130						135					140					
gtg	gag	ggg	ctg	tac	ttg	cac	agc	ctc	atc	ttc	atg	gcc	ttt	ttc	tca	480
Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	
145						150					155			160		
gag	aag	aag	tac	ctg	tgg	ggc	ttc	acc	atc	ttt	ggc	tgg	ggt	cta	ccg	528
Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Ile	Phe	Gly	Trp	Gly	Leu	Pro	
165								170					175			
gct	gtc	ttc	gtg	gct	gtg	tgg	gtc	ggt	gtc	aga	gca	acc	ttg	gcc	aac	576
Ala	Val	Phe	Val	Ala	Val	Trp	Val	Gly	Val	Arg	Ala	Thr	Leu	Ala	Asn	
180								185					190			
act	ggg	tgc	tgg	gat	ctg	agc	tcc	ggg	cac	aag	aag	tgg	atc	atc	cag	624
Thr	Gly	Cys	Trp	Asp	Leu	Ser	Ser	Gly	His	Lys	Lys	Trp	Ile	Ile	Gln	
195								200					205			
gtg	ccc	atc	ctg	gca	tct	gtt	gtg	ctc	aac	ttc	atc	ctt	ttt	atc	aac	672
Val	Pro	Ile	Leu	Ala	Ser	Val	Val	Leu	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
210							215					220				
atc	atc	cgg	gtg	ctt	gcc	act	aag	ctt	cgg	gag	acc	aat	gcg	ggc	cg	720
Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	
225							230					235			240	
tgt	gac	acc	agg	cag	cag	tac	cg	aag	ctg	ctc	agg	tcc	acg	ttg	gtg	768
Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Arg	Ser	Thr	Leu	Val	
245								250					255			

ctc gtg ccg ctc ttt ggt gtg cac tac acc gtc ttc atg gcc ttg ccg	816		
Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro			
260	265	270	
tac acc gag gtc tca ggg aca ttg tgg cag atc cag atg cat tat gag	864		
Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu			
275	280	285	
atg ctc ttc aac tcc ttc cag gga ttt ttt gtt gcc atc ata tac tgt	912		
Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys			
290	295	300	
ttc tgc aat ggt gag gtg cag gca gag att agg aag tca tgg agc cgc	960		
Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg			
305	310	315	320
tgg aca ctg gcg tag	975		
Trp Thr Leu Ala			

<210> 41  
<211> 324  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<400> 41  
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys  
1 5 10 15  
Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly  
20 25 30  
Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val  
35 40 45  
Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn  
50 55 60  
Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser  
65 70 75 80  
Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu  
85 90 95  
Ala Glu Arg Leu Thr Glu Glu Leu His Ile Ile Ala Gln Val Pro  
100 105 110  
Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala  
115 120 125  
Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu  
130 135 140  
Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser  
145 150 155 160  
Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro  
165 170 175  
Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn  
180 185 190  
Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln  
195 200 205  
Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn  
210 215 220  
Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg  
225 230 235 240  
Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val

245	250	255
Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro		
260	265	270
Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu		
275	280	285
Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys		
290	295	300
Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg		
305	310	315
Trp Thr Leu Ala		320

<210> 42  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> UNSURE  
<222> (1)..(1)  
<223> May be any amino acid.

<220>  
<221> UNSURE  
<222> (3)..(3)  
<223> May be any amino acid.

<220>  
<221> UNSURE  
<222> (5)..(8)  
<223> May be any amino acid.

<220>  
<223> Description of Artificial Sequence: synthetic  
polypeptide

<400> 42  
Xaa Val Xaa Glu Xaa Xaa Xaa Xaa His  
1 5

<210> 43  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> UNSURE  
<222> (1)..(5)  
<223> May be any amino acid.

<220>  
<221> UNSURE  
<222> (7)..(8)  
<223> May be any amino acid.

<220>  
<221> UNSURE  
<222> (10)  
<223> May be any amino acid.

<220>  
<221> UNSURE  
<222> (12)  
<223> May be any amino acid.

<220>  
<221> UNSURE  
<222> (15)..(16)  
<223> May be any amino acid.

<220>  
<223> Description of Artificial Sequence: synthetic  
Polypeptide

<400> 43  
Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Trp Xaa Leu Xaa Lys Leu Xaa Xaa  
1 5 10 15

Val

<210> 44  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 44  
Ser Val Ser Glu Ile Gln Leu Met His  
1 5

<210> 45  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 45  
Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln  
1 5 10 15

Asp Val

<210> 46  
<211> 120  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<220>  
<221> CDS  
<222> (1)..(120)

<400> 46  
atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc  
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys  
1 5 10 15

cca gtg ctc agc tcc gca tat gcg ctg gtg gat gcg gac gat gtc ttt 96  
Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Phe  
20 25 30

acc aaa gag gaa cag att ttc ctg 120  
Thr Lys Glu Glu Gln Ile Phe Leu  
35 40

<210> 47  
<211> 120  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<220>  
<221> CDS  
<222> (1)...(120)

<400> 47 48  
aac cgg acg tgg gcc aac tac agc gag tgc ctc aag ttc atg acc aat  
Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn  
1 5 10 15

gag acc cgg gaa cgg gag gta ttt gac cgc cta ggc atg atc tac acc 96  
Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr  
20 25 30

gtg gga tac tcc atg tct ctc gcc 120  
Val Gly Tyr Ser Met Ser Leu Ala  
35 40

<210> 48  
<211> 39  
<212> RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<400> 48 39  
gcuguuuccg aaauccagcu gaugcacggc ggaggaggc

<210> 49  
<211> 99  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<400> 49 60  
ctctgctgcc cagtgctcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 99  
ggaggaggcg aggtatttga ccgcctaggc atgatctac

```
<210> 50
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> modified PTH receptor sequence

<220>
<221> misc_feature
<222> (1)..(30)
<223> flanking region

<220>
<221> misc_feature
<222> (31)..(69)
<223> insert

<220>
<221> misc_feature
<222> (70)..(99)
<223> flanking region

<220>
<221> CDS
<222> (1)..(99)

<400> 50
ctc tgc tgc cca gtg ctc agc tcc gcc tat gcg gtt tcc gaa atc cag 48
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln
1 5 10 15
ctg atg cac ggc gga ggc gag gta ttt gac cgc cta ggc atg atc 96
Leu Met His Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile
20 25 30
tac 99
Tyr

<210> 51
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      oligonucleotide

<400> 51
ctctgctgcc cagtgcgtcag ctccgcataat ccctacgacg tcccccacta cgccggcgga 60
ggaggcgagg tatttgaccg cctaggcatg atctac 96

<210> 52
<211> 96
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: modified PTH  
sequence

<220>  
<221> misc\_feature  
<222> (28)..(54)  
<223> insert

<220>  
<221> CDS  
<222> (1)..(96)

<400> 52  
ctc tgc tgc cca gtg ctc agc tcc gca tat ccc tac gac gtc ccc gac 48  
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Pro Tyr Asp Val Pro Asp  
5 10 15  
1  
tac gcc ggc gga gga ggc gag gta ttt gac cgc cta ggc atg atc tac 96  
Tyr Ala Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr  
20 25 30

<210> 53  
<211> 40  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 53  
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys 5 10 15  
1  
Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Phe  
20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu  
35 40

<210> 54  
<211> 40  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 54  
Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn 5 10 15  
1  
Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr  
20 25 30

Val Gly Tyr Ser Met Ser Leu Ala  
35 40

<210> 55  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 55  
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln  
1 5 10 15  
Leu Met His Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile  
20 25 30

Tyr

<210> 56  
<211> 32  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 56  
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Pro Tyr Asp Val Pro Asp  
1 5 10 15  
Tyr Ala Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr  
20 25 30

<210> 57  
<211> 1380  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<220>  
<221> CDS  
<222> (1)..(1353)

<400> 57 48  
atg ggg acc gcc cgg atc gca ccc ggc ctg gcg ctc ctg ctc tgc tgc  
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys  
1 5 10 15  
ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cat 96  
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His  
20 25 30

aat cgt ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac	144
Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr	
35 40 45	
acc gtg ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc	192
Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu	
50 55 60	
atc ctg gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac	240
Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His	
65 70 75 80	
atg cac ctg ttc ctg tcc atg ctg cgc gcc gtg agc atc ttc gtc	288
Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val	
85 90 95	
aag gac gct gtg ctc tac tct ggc acg ctt gat gag gct gag cgc	336
Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg	
100 105 110	
ctc acc gag gag ctc ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct	384
Leu Thr Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro	
115 120 125	
gcc acc gcc gct gcc ggc tac ggc tgc agg gtg gct gtg acc ttc	432
Ala Thr Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe	
130 135 140	
ttc ctt tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg	480
Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly	
145 150 155 160	
ctg tac ctg cac agc ctc atc ttc atg gcc ttc ttc tca gag aag aag	528
Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys	
165 170 175	
tac ctg tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc	576
Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe	
180 185 190	
gtg gct gtg tgg gtc agt gtc aga gct acc ctg gcc aac acc ggg tgc	624
Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys	
195 200 205	
tgg gac ttg agc tcc ggg aac aaa aag tgg atc atc cag gtg ccc atc	672
Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile	
210 215 220	
ctg gcc tcc att gtg ctc aac ttc atc ctc ttc atc aat atc gtc cgg	720
Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg	
225 230 235 240	
gtg ctc gcc acc aag ctg cgg gag acc aac gcc ggc cgg tgt gac aca	768
Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr	
245 250 255	
cgg cag cag tac cgg aag ctg ctc aaa tcc acg ctg gtg ctc atg ccc	816
Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro	
260 265 270	
ctc ttt ggc gtc cac tac att gtc ttc atg gcc aca cca tac acc gag	864
Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu	

275	280	285	
gtc tca ggg acg ctc tgg caa gtc cag atg cac tat gag atg ctc ttc			912
Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe			
290	295	300	
aac tcc ttc cag gga ttt ttt gtc gca atc ata tac tgt ttc tgc aat			960
Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn			
305	310	315	320
ggc gag gta caa gct gag atc aag aaa tct tgg agc cgc tgg aca ctg			1008
Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu			
325	330	335	
gca ctg gac ttc aag cga aag gca cgc agc ggg agc agc agc tat agc			1056
Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser			
340	345	350	
tac ggc ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt			1104
Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg			
355	360	365	
gtg gga ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc			1152
Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr			
370	375	380	
acc aac ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca			1200
Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro			
385	390	395	400
gcc ctg gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag			1248
Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys			
405	410	415	
gac gat ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc			1296
Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala			
420	425	430	
tct ggg cct gag cgg cca cct gcc ctg cta cag gaa gag tgg gag aca			1344
Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr			
435	440	445	
gtc atg tga ccaggcgctg gggctggac ctgctga			1380
Val Met			
450			

<210> 58  
<211> 450  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<400> 58  
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys  
1 5 10 15  
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His  
20 25 30  
Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr

35	40	45
Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu		
50	55	60
Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His		
65	70	75
80		
Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val		
85	90	95
Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg		
100	105	110
Leu Thr Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro		
115	120	125
Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe		
130	135	140
Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly		
145	150	155
160		
Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys		
165	170	175
Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe		
180	185	190
Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys		
195	200	205
Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile		
210	215	220
Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg		
225	230	235
240		
Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr		
245	250	255
Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro		
260	265	270
Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu		
275	280	285
Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe		
290	295	300
Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn		
305	310	315
320		
Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu		
325	330	335
Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser		
340	345	350
Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg		
355	360	365
Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr		
370	375	380
Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro		
385	390	395
400		
Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys		
405	410	415
Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala		
420	425	430
Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr		
435	440	445
Val Met		
450		

<210> 59  
<211> 1380  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<220>

<221> CDS

<222> (28) .. (1335)

<400> 59  
tggatccgc ggcccttaggc ggtggcg atg ggg acc gcc cg<sup>54</sup>  
Met Gly Thr Ala Arg Ile Ala Pro Gly  
1 5  
ctg g<sup>102</sup> g<sup>102</sup> c<sup>102</sup> c<sup>102</sup> t<sup>102</sup> c<sup>102</sup> t<sup>102</sup> g<sup>102</sup> c<sup>102</sup> a<sup>102</sup> t<sup>102</sup> g<sup>102</sup> a<sup>102</sup> g<sup>102</sup> t<sup>102</sup>  
Leu Ala Leu Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Glu Val  
10 15 20 25  
ttt g<sup>150</sup> a<sup>150</sup> c<sup>150</sup> g<sup>150</sup> c<sup>150</sup> t<sup>150</sup> g<sup>150</sup> a<sup>150</sup> t<sup>150</sup> c<sup>150</sup> t<sup>150</sup> g<sup>150</sup> t<sup>150</sup> c<sup>150</sup> t<sup>150</sup>  
Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu  
30 35 40  
g<sup>198</sup> c<sup>198</sup> t<sup>198</sup> c<sup>198</sup> a<sup>198</sup> c<sup>198</sup> g<sup>198</sup> t<sup>198</sup> a<sup>198</sup> g<sup>198</sup> c<sup>198</sup> t<sup>198</sup> t<sup>198</sup> a<sup>198</sup> g<sup>198</sup> g<sup>198</sup> c<sup>198</sup> t<sup>198</sup>  
Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu  
45 50 55  
c<sup>246</sup> a<sup>246</sup> t<sup>246</sup> g<sup>246</sup> c<sup>246</sup> a<sup>246</sup> c<sup>246</sup> t<sup>246</sup> a<sup>246</sup> c<sup>246</sup> a<sup>246</sup> t<sup>246</sup> g<sup>246</sup> c<sup>246</sup> t<sup>246</sup> t<sup>246</sup> a<sup>246</sup> t<sup>246</sup>  
His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met  
60 65 70  
c<sup>294</sup> t<sup>294</sup> g<sup>294</sup> c<sup>294</sup> g<sup>294</sup> t<sup>294</sup> a<sup>294</sup> g<sup>294</sup> a<sup>294</sup> c<sup>294</sup> g<sup>294</sup> t<sup>294</sup> c<sup>294</sup> t<sup>294</sup> a<sup>294</sup> c<sup>294</sup> t<sup>294</sup> g<sup>294</sup>  
Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly  
75 80 85  
g<sup>342</sup> c<sup>342</sup> a<sup>342</sup> c<sup>342</sup> t<sup>342</sup> g<sup>342</sup> a<sup>342</sup> g<sup>342</sup> c<sup>342</sup> g<sup>342</sup> a<sup>342</sup> g<sup>342</sup> g<sup>342</sup> a<sup>342</sup> g<sup>342</sup> c<sup>342</sup> g<sup>342</sup> c<sup>342</sup> g<sup>342</sup>  
Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala  
90 95 100 105  
a<sup>390</sup> t<sup>390</sup> c<sup>390</sup> a<sup>390</sup> g<sup>390</sup> c<sup>390</sup> c<sup>390</sup> g<sup>390</sup> c<sup>390</sup> t<sup>390</sup> g<sup>390</sup> c<sup>390</sup> a<sup>390</sup> c<sup>390</sup> g<sup>390</sup> t<sup>390</sup> a<sup>390</sup> c<sup>390</sup> g<sup>390</sup>  
Ile Ala Gln Ala Pro Pro Pro Ala Thr Ala Ala Ala Gly Tyr Ala  
110 115 120  
g<sup>438</sup> c<sup>438</sup> t<sup>438</sup> g<sup>438</sup> a<sup>438</sup> g<sup>438</sup> g<sup>438</sup> t<sup>438</sup> c<sup>438</sup> t<sup>438</sup> t<sup>438</sup> a<sup>438</sup> c<sup>438</sup> t<sup>438</sup> g<sup>438</sup> c<sup>438</sup> a<sup>438</sup> a<sup>438</sup>  
Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn  
125 130 135  
t<sup>486</sup> a<sup>486</sup> c<sup>486</sup> t<sup>486</sup> g<sup>486</sup> a<sup>486</sup> g<sup>486</sup> g<sup>486</sup> t<sup>486</sup> c<sup>486</sup> t<sup>486</sup> a<sup>486</sup> c<sup>486</sup> t<sup>486</sup> a<sup>486</sup> t<sup>486</sup>  
Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe  
140 145 150  
a<sup>534</sup> t<sup>534</sup> g<sup>534</sup> c<sup>534</sup> t<sup>534</sup> t<sup>534</sup> c<sup>534</sup> a<sup>534</sup> g<sup>534</sup> a<sup>534</sup> g<sup>534</sup> t<sup>534</sup> c<sup>534</sup> a<sup>534</sup> g<sup>534</sup> t<sup>534</sup> t<sup>534</sup>  
Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe  
155 160 165  
g<sup>582</sup> c<sup>582</sup> t<sup>582</sup> g<sup>582</sup> c<sup>582</sup> g<sup>582</sup> t<sup>582</sup> c<sup>582</sup> t<sup>582</sup> g<sup>582</sup> c<sup>582</sup> t<sup>582</sup> g<sup>582</sup> t<sup>582</sup> a<sup>582</sup> g<sup>582</sup> t<sup>582</sup> a<sup>582</sup> g<sup>582</sup>  
Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg  
170 175 180 185  
g<sup>630</sup> c<sup>630</sup> t<sup>630</sup> g<sup>630</sup> a<sup>630</sup> a<sup>630</sup> c<sup>630</sup> a<sup>630</sup> c<sup>630</sup> g<sup>630</sup> t<sup>630</sup> g<sup>630</sup> a<sup>630</sup> c<sup>630</sup> g<sup>630</sup> a<sup>630</sup> a<sup>630</sup>  
Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys  
190 195 200  
a<sup>678</sup> t<sup>678</sup> g<sup>678</sup> a<sup>678</sup> t<sup>678</sup> c<sup>678</sup> a<sup>678</sup> c<sup>678</sup> g<sup>678</sup> t<sup>678</sup> c<sup>678</sup> t<sup>678</sup> a<sup>678</sup> a<sup>678</sup> t<sup>678</sup> c<sup>678</sup> a<sup>678</sup> t<sup>678</sup>  
Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe

205	210	215	
atc ctc ttc atc aat atc gtc cggtc ctc gcc acc aag ctg cggtc gag			726
Ile Leu Phe Ile Asn Ile Val Arg Val Leu Ala Thr Lys Leu Arg Glu			
220	225	230	
acc aac gcc ggc cggtc tgt gac aca cggtc cag cag tac cggtc aag ctg ctc			774
Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu			
235	240	245	
aaa tcc acg ctg gtgc ttc atgc ccc ctc ttt ggc gtc cac tac att gtc			822
Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val			
250	255	260	265
ttc atg gcc aca cca tac acc gag gtc tca ggg acg ctc tgg caa gtc			870
Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Val			
270	275	280	
cag atg cac tat gag atg ctc ttc aac tcc ttc cag gga ttt ttt gtc			918
Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val			
285	290	295	
gca atc ata tac tgt ttc tgc aat ggc gag gta caa gct gag atc aag			966
Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys			
300	305	310	
aaa tct tgg agc cgc tgg aca ctg gca ctg gac ttc aag cga aag gca			1014
Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala			
315	320	325	
cgc agc ggg agc agc agc tat agc tac ggc ccc atg gtgc tcc cac aca			1062
Arg Ser Gly Ser Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr			
330	335	340	345
agt gtgc acc aat gtc ggc ccc cgt gtgc gga ctc ggc ctg ccc ctc agc			1110
Ser Val Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser			
350	355	360	
ccc cgc cta ctg ccc act gcc acc acc aac ggc cac cct cag ctg cct			1158
Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn Gly His Pro Gln Leu Pro			
365	370	375	
ggc cat gcc aag cca ggg acc cca gcc ctg gag acc ctc gag acc aca			1206
Gly His Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr			
380	385	390	
cca cct gcc atg gct ccc aag gac gat ggg ttc ctc aac ggc tcc			1254
Pro Pro Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Asn Gly Ser			
395	400	405	
tgc tca ggc ctg gac gag gag gcc tct ggg cct gag cggtc cca cct gcc			1302
Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Pro Glu Arg Pro Pro Ala			
410	415	420	425
ctg cta cag gaa gag tgg gag aca gtc atg tga ccaggcgctg ggggtggac			1355
Leu Leu Gln Glu Glu Trp Glu Thr Val Met			
430	435		
ctgctgacat agtggatgga cagat			1380

<211> 435  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<400> 60  
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys  
1 5 10 15  
Pro Val Leu Ser Ser Ala Tyr Glu Val Phe Asp Arg Leu Gly Met Ile  
20 25 30  
Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val  
35 40 45  
Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile  
50 55 60  
His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe  
65 70 75 80  
Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu  
85 90 95  
Arg Leu Thr Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro  
100 105 110  
Pro Ala Thr Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr  
115 120 125  
Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu  
130 135 140  
Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys  
145 150 155 160  
Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val  
165 170 175  
Phe Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly  
180 185 190  
Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro  
195 200 205  
Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val  
210 215 220  
Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp  
225 230 235 240  
Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met  
245 250 255  
Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr  
260 265 270  
Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu  
275 280 285  
Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys  
290 295 300  
Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr  
305 310 315 320  
Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Tyr  
325 330 335  
Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro  
340 345 350  
Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala  
355 360 365  
Thr Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr  
370 375 380  
Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro  
385 390 395 400  
Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu  
405 410 415

Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu  
 420 425 430  
 Thr Val Met  
 435

<210> 61  
 <211> 1363  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: modified PTH  
 receptor sequence

<220>  
 <221> CDS  
 <222> (1)..(1347)

<400> 61	48
atg ggg acc gcc cgg atc gca ccc ggc ctg gcg ctc ctg ctc tgc tgc	
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys	
1 5 10 15	
ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cac	96
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His	
20 25 30	
ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac acc gtg	144
Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val	
35 40 45	
ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc atc ctg	192
Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu	
50 55 60	
gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac	240
Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His	
65 70 75 80	
ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc aag gac	288
Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp	
85 90 95	
gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc ctc acc	336
Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr	
100 105 110	
gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg cct gcc acc	384
Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Ala Thr	
115 120 125	
gcc gct gcc ggc tac gcg ggc tgc agg gtg gct gtg acc ttc ttc ctt	432
Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu	
130 135 140	
tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg ctg tac	480
Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr	
145 150 155 160	
ctg cac agc ctc atc ttc atg gcc ttc tca gag aag aag tac ctg	528

Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu			
165	170	175	
tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc gtg gct	576		
Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala			
180	185	190	
gtg tgg gtc agt gtc aga gct acc ctg gcc aac acc ggg tgc tgg gac	624		
Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp			
195	200	205	
ttg agc tcc ggg aac aaa aag tgg atc atc cag gtg ccc atc ctg gcc	672		
Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala			
210	215	220	
tcc att gtg ctc aac ttc atc ctc ttc atc aat atc gtc cgg gtg ctc	720		
Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu			
225	230	235	240
gcc acc aag ctg cgg gag acc aac gcc ggc cgg tgt gac aca cgg cag	768		
Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln			
245	250	255	
cag tac cgg aag ctg ctc aaa tcc acg ctg gtg ctc atg ccc ctc ttt	816		
Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe			
260	265	270	
ggc gtc cac tac att gtc ttc atg gcc aca cca tac acc gag gtc tca	864		
Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser			
275	280	285	
ggg acg ctc tgg caa gtc cag atg cac tat gag atg ctc ttc aac tcc	912		
Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser			
290	295	300	
ttc cag gga ttt ttt gtc gca atc ata tac tgt ttc tgc aat ggc gag	960		
Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu			
305	310	315	320
gta caa gct gag atc aag aaa tct tgg agc cgc tgg aca ctg gca ctg	1008		
Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu			
325	330	335	
gac ttc aag cga aag gca cgc agc ggg agc agc agc tat agc tac ggc	1056		
Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Tyr Ser Tyr Gly			
340	345	350	
ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt gtg gga	1104		
Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly			
355	360	365	
ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc acc aac	1152		
Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn			
370	375	380	
ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca gcc ctg	1200		
Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu			
385	390	395	400
gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag gac gat	1248		
Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp			
405	410	415	

ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc tct ggg	1296
Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly	
420	425
430	
cct gag cg <sup>g</sup> cca cct gcc ctg cta cag gaa gag tgg gag aca gtc atg	1344
Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met	
435	440
445	
tga ccaggcgctg ggggct	1363

<210> 62  
<211> 448  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
receptor sequence

<400> 62  
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys  
1 5 10 15  
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His  
20 25 30  
Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val  
35 40 45  
Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu  
50 55 60  
Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His  
65 70 75 80  
Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp  
85 90 95  
Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr  
100 105 110  
Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr  
115 120 125  
Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu  
130 135 140  
Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr  
145 150 155 160  
Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu  
165 170 175  
Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala  
180 185 190  
Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp  
195 200 205  
Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala  
210 215 220  
Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu  
225 230 235 240  
Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln  
245 250 255  
Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe  
260 265 270  
Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser  
275 280 285  
Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser  
290 295 300  
Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu  
305 310 315 320

Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu  
325 330 335  
Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly  
340 345 350  
Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly  
355 360 365  
Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn  
370 375 380  
Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu  
385 390 395 400  
Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp  
405 410 415  
Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly  
420 425 430  
Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met  
435 440 445

<210> 63  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 63  
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val  
1 5 10 15

<210> 64  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 64  
Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Ile Gln  
1 5 10 15  
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile  
20 25 30

<210> 65  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 65  
Ala Val Ser Glu His Gly Gly Gly Gly Gly Gly Gly Gly Ile Gln  
1 5 10 15  
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile  
20 25 30

<210> 66

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 66

Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Gly Gly  
1 5 10 15

Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile  
20 25 30

<210> 67

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH  
sequence

<400> 67

Ala Val Ser Glu Ile Gln Leu Met His Asn Leu  
1 5 10

<210> 68

<211> 99

<212> DNA

<213> Artificial sequence

<220>

<223> modified PTH sequence

<400> 68

ctctgctgcc ccgtgcttag ctccgcgtac gcgggttccg aaatccagct gatgcacggc 60

ggaggaggcg aggtgtttga ccgcctgggc atgatttac 99

<210> 69

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> modified PTH receptor sequence

<220>

<221> CDS

<222> (3) .. (47)

<400> 69

cc gaa atc cag ctg atg cat aat cgt ggc gga ggc gag gtg ttt g 48

Glu Ile Gln Leu Met His Asn Arg Gly Gly Gly Gly Glu Val Phe  
1 5 10 15

<210> 70  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> modified PTH receptor sequence

<400> 70

Glu Ile Gln Leu Met His Asn Arg Gly Gly Gly Gly Glu Val Phe Asp  
1 5 10 15

<210> 71  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 71

Pro Tyr Asp Val Pro Asp Tyr Ala  
1 5

<210> 72  
<211> 13  
<212> PRT  
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<220>  
<223> modified PTH receptor sequence

<400> 72

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly  
1 5 10

<210> 73  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 73

Ala Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His  
1 5 10

*B*  
<210> 74  
<211> 9  
<212> PRT  
<213> Rattus sp.

<400> 74  
Ala Val Ser Glu Ile Gln Leu Met His  
1 5